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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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    May 18, 2002, 04:47:34; Search time 116.57 Seconds (without alignments) 534.256 Million cell updates/sec
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1 MEPFKQQKVEDFY
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Copyright (c) 1993 - 2000 Compugen Ltd.
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O75892 homo sapien
O9911k4 homo sapien
O991yM4 mus musculu
O88861 mus musculu
O91jp7 mus musculu
O91jp7 mus musculu
O91jp7 mus musculu
O92044 mus musculu
O43293 homo sapien
O54784 mus musculu
O43293 homo sapien
O54784 mus musculu
O43293 homo sapien
O54784 mus musculu
O88764 rattus norv
O44997 caenorhabdi
O90615 homo sapien
O91be69 macaca fasc
O98850 carassius a
O91xs9 cavia porce
P91255 caenorhabdi
                                                                                                                                                                                      Description
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008767 rattus norv	mus mu	O70150 rattus norv		drosc	Q9hd31 homo sapien	mytilus		Q95sk9 drosophila	_		Q23551 caenorhabdi	Q23550 caenorhabdi	_				Q9gv79 drosophila			-	Q9h1r3 homo sapien		Q96dv1 homo sapien	~	076281 drosophila	Q91xs8 rattus norv		Q961ul drosophila

ALIGNMENTS

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                                                                                                                        RESULT
075892
                                                      Query Match
Best Local
                                  Matches 359;
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                                                                                                             Pfam; PF00069; pkinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; ATP-binding; Kinase; Serine/threonine-protein kinase; SEQUENCE 370 AA; 42923 MW; 09502B4ADCD20F91 CRC64;
                                                                                                                                                                                                                                                                            MEDLINE-20094983; PubMed-10629061;
Inbal B., Shani G., Cohen O., Kissil J.L., Kimchi A.;
Inbal B., Shani G., Cohen O., Kissil J.L., Kimchi A.;
"Death-associated protein kinase-related protein 1, a novel
Serine/Threonine kinase involved in apoptosis.";
Mol. Cell. Biol. 20:1044-1054(2000).

-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AR052941; AAC35001.1; -.
EMBL; OB3450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                             InterPro; IPR002719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                    Local
                                                   Similarity
                                  Conservative
                                                 99.4%;
99.7%;
                                  0,
                                Score 1835; DB 4;
Pred. No. 3.2e-125;
0; Mismatches 1;
                                                               Length 370;
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1 Oncogene 18:3471-3480(1999).

1 Oncogene 18:3471-3480(1999).

2 Oncogene 18:3471-3480(1999).

3 Oncogene 18:3471-3480(1999).

3 R EMBL; ABOLBOO1; BAAB8063.1;

3 R EMBL; ABOLBOO1; BAAB8063.1;

4 R HSSP; O63450; 1A06.

5 R HSSP; O63450; 1A06.

7 R HSSP; O63450; 1A06.

7 R HSSP; O63450; 1A06.

7 R InterPro; IPR002290; Ser_thr_pkinase.

8 InterPro; IPR002290; Ser_thr_pkinase.

9 InterPro; IPR001245; Tyr_pkinase.

9 FAINTS; PF00019; PKINASE; 1.

9 PAINTS; PF000109; TYRKINASE.

9 PAINTS; PF000109; TYRKINASE_DOM; 1.

9 PROSITE; PS001010; PROTEIN_KINASE_DOM; 1.

9 PROSITE; PS001010; PROTEIN_KINASE_ST: 1.
                                                                                                                                                                                           Matches
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Q9UIK4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
DEATH-ASSOCIATED PROTEIN KINASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-99303018; PubMed-10376525;

KRAWAI T., Nomura F., Hoshino K., Copeland N.G.,

Jenkins N.A., Akira S.;

"Death-associated protein kinase 2 is a new calc

"Death-associated protein kinase 2 is a new calc

dependent protein kinase that signals apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; (
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1; Mismatches
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No. 2e-124;
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Best Local Similarity
Matches 347; Conserv
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01-mAY-2000 (TrEMBLrel. 13, Last sequence update)
01-mAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DEATH-ASSOCIATED PROTEIN KINASE 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9QYM4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR00719; Euk_pkinase.
Interpro; IPR002290; Ser_thr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
pfam; PF00069; pkinase: 1.
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                                                                                                                                                                                                                                                                                                                                          PRINTS: PRO0109; TYRKINASE.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS500101; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 370 AA; 42769 MW; 7DA6E29C4E6615B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRRRWKLSFSIVSLCNHLTRSLMKKVHLRPDEDLRNCESDTEEDIARRKALHPRRRSSTS
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                                                                                                                                                             METFKQQKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVCREE
                                                                                                                                                                                   MEPFKQQKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREE
PRELIMINARY;
                                                                                                                                                                                                                                              95.6%; Score 1764; DB 11;
ilarity 96.4%; Pred. No. 4.4e-120;
Conservative 4; Mismatches 9;
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Sciurognathi; Muridae; Murinae; Mus
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apoptosis through its catalytic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 96.0 Matches 291; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DAP-KINASE RELATED PROTEIN 1 (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0109; TYRKINASE.

PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
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[1]
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  STS
                                                                                                                                   EEFFSHTSELAKDFIRKLLVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLENFR
                                                                                                                                                                                                                              FGTPEFVAPEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFD
                                           KQYVRRRWKLSFSIVSLCNHLTRSLMKKVHLRPDEDLRNCESDTEEDIARRKALHPRRRS
                                                                                                                                                                                                                                                                                                                             SFIKQILDGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNI
                                                                                                                                                                                                                                                                                                                                                     SFIKQILDGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNI
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4; Mismatche
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R Pfam; PF000069; pkinase; 1.

R SMART; SM00248; ANK; 8.

R SMART; SM00205; DEATH; 1.

R SMART; SM00205; DEATH; 1.

R PROSITE; PS50088; ANK_REPEAT; 7.

R PROSITE; PS50017; DEATH_DOMAIN; 1.

R PROSITE; PS50017; DEATH_DOMAIN; 1.

R PROSITE; PS50017; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS50011; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

W ANK repeat; ATP-binding; Kinase; Repeat;

W Serine/threonine-protein kinase; Transferase.

SEQUENCE 1430 AA; 159843 MW; 81C8356CDD14BBE8 CRC64;
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1996) to the EMBL/GenBank/DDBJ: SIMILARITY: BELONGS TO THE SER/THR FAMILY EMBL; X97048; CAA65762.1; -. HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000488; Death
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Kimchi A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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 301
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                                                                                                                                                                                                                                                                                                                           Local Similarity hes 244; Conserv
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ARKKWKQSVRLISLCQRLSRSFLSRSNMSVARSDDTL---
                                                                                                                                                                          KQILDGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGT
                                                                                                                                                                                                                                IEREVSILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFI
                          VRRRWKLSFSIVSLCNHLTRSLMKKVHL - - - RPDEDLRNCESDTEEDIARRKALH
                                                                                                                                                            KQILSGVYYLHSLQIAHFDLKPENIMLLDRNVPKPRIKIIDFGLAHKIDFGNEFKNIFGT
                                                                                                                                                                                                                   IEREVSILKEIRHPNVITLHEVYENKTDVILILELVAGGELFDFLAEKESLTEEEATEFL
                                                                                                                                                                                                                                                                      MTVFRQENVDDYYDTGEELGSGQFAVVKKCREKSTGLQYAAKFIKKRRTKSSRRGVSRED
                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                        70.3%;
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Pred. No. 1.9e
58; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      DB 11;
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OF PROTEI
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Strausberg R.;

Strausberg R.;

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

C. -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

C. -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

C. EMBL; BC003614: AAH03614.1; --

C. EMBL; BC003614: AAH03614.1;

C. EMBL; BC003614: AAH03614.1;

C. EMBL; BC003614: AAH03614.1;

C. EMBL; BC003614: AAH0
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Best Local S
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OSBTL8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO DEATH-ASSOCIATED PROTEIN KINASE 1.

Homo sapiens (Human). Chardets. Craniata: Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                               Q9CV44

Q9CV44;
Q9CV44;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence up
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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          Eukaryota;
                                        Mus musculus (Mouse)
                                                                           2310039H24RIK
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nes 242; Conserv
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          Metazoa;
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                 Chordata;
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pred. No. 6.1e-86;
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                    Craniata;
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RRA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RRA Arzakwa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,
RRA Arzakwa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RRA Arzakwa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RRA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RRA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RRA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RRA Kuchl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
RRA Kuchl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
RRA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RRA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RRA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RRA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RRA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RRA Wynshaw-Boris A., Yoshida K., Wang K.H., Waitzacelli J., Mombaerts P.,
RRA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RRA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RRA Hayashizaki Y.,
RRA Hayashizaki Y., Jane J., Marinase.
DR HSSP, G63450; 1A06.
DR HSSP, G63450; 1A06.
DR HSSP, G63450; 1A06.
DR HSSP, G63450; 1A06.
DR PROSITE; PS00109; TYRKINASE.
DR PRINTS; PR00109; TYRKINASE.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR SMART; SM00220; Ser_thr_pkinase.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00117; PROTEIN_KINASE_DOM; 1.
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MEDLINE-21085660; PubMed-11217851;
Kawai J., Shinagawa A., Shibata K.
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NCBI_TaxID=10090;
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NON_TER 345 345
SEQUENCE 345 AA; 39776
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                                                    301 VRRRWKLSFSIVSLCNHL 318
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                                                                                                              FRNTSTLAKDFTRRLLVKDPKKRMTIQDSLQHPWIKPKDTQQALSRKASAVNMEKFKRFA
                                                                                                                                                FSHTSELAKDEIRKLLVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLENFRKQY
   ARKKWK---
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Best Local S
Matches 233
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043293;
01-JUN-1998
01-JUN-1998
01-OCT-2001
ZIP-KINASE.
                                                                                                                                                                                                                                                                                                                   InterPro; LYNOVALO, Pfam; PFO0069; PKINASE; I.

Pfam; PF00069; PKINASE; I.

SMARP; SM00220; S_TKC; 1.

SMARP; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99283879; PubMed=10356987;
Murata-Hori M., Suizu F., Iwasaki
"ZIP kinase identified as a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98147805; PubMed=9488481;
Kawai T., Matsumoto M., Takeda K., Sanjo H.,
"ZIP kinase, a novel serine/threonine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in HeLa cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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es 233; Conservative
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                    9
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                                                                                              FSHTSELAKDFIRKLLVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLENFRKQY
                                                                                                                         FSNTSELAKDFIRRLLVKDPKRRMTIAQSLEHSWI-----KAIRRRNVRGEDSGRKPE
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3 (TrEMBLrel. 06,
1 (TrEMBLrel. 18,
 PRELIMINARY;
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Last sequence up
Last annotation
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Pred. No. 1.3e-76;
9; Mismatches 60
 PRT;
                                               LPPNNSYADFERFSKVLEEAAAAEEGLRELQRS
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myosin regulatory light
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Best Local Similarity
Matches 225; Conserv
                                                                   088764;
0088764;
01-NOV-1998;
01-NOV-1998;
01-DEC-2001;
DAP-LIKE KIN;
DLK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00069; pkinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threeprotein kinase; PS00108; PROSITE; PS00108; PROTEIN_KINASE_ST; DA32EF3EB1F20EFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE SER/TH
EMBL; AB007143; BAA24954.1; -.
HSSP; Q63450; 1A06.
MGD; MGI:1203520; Dapk3.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis."
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MEDLINE-98147805; PubMed-9488481;
Kawai T., Matsumoto M., Takeda K., Sanjo H.,
"ZIP-kinase, a novel serine/threonine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                                                                                     PRELIMINARY;
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71.0%;
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                                                                                                             Created)
Last sequence
Last annotation
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Last sequence update)
Last annotation update)
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Pred. No. 9.7e-75;
8; Mismatches 42;
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Craniata; Vertebrata; | Sciurognathi; Muridae;
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annotation
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mediates
                         Euteleostomi;
    Murinae;
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Oncogene 20:2645-2654(1998).

CONCOGENE 20:2645-2654(1998).

CONCOGENE 20:2645-2654(1998).

CONCOGENE 20:2645-2654(1998).

REMBL; AJ006971; CAA07360.1; -.

REMBL; AJ006971; Euk_pkinase.

InterPro; IPR002290; Ser_thr_pkinase.

RINTERPOOSITE; PR002290; Ser_thr_pkinase.

PEGAMET; SM002209; S_TKC; 1.

REMBL; AJ006971; PROTEIN_KINASE_ATP; 1.

REMBL; AJ006971; PROTEIN_KINASE_DOM; 1.

REMBL; AJ006971; PROTEIN_KINASE_DOM; 1.

REMBL; AJ006971; PROTEIN_KINASE_ST; 
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Best Local S
Matches 225
                                                                                                                                                                                                                                                                                                                                       O44997 PRELIMINARY;
O44997;
O1-JUN-1998 (TrEMBLrel. (
O1-JUN-1998 (TrEMBLrel. (
O1-DEC-2001 (TrEMBLrel. (
KIZCII.4 PROTEIN. (
KIZCII.4 Caenorhabditis elegans. (
Caenorhabditis elegans.
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Kogel D., Plottner O., Landsberg G., Christian Cloning and Characterisation of Dlk, a novel s "Cloning and characterisation of the annual report of the chromatin and F that is tightly associated with chromatin and F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
[1]
"Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consort Science 282:2012-2018(1998).
                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nemata
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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mes 225; Conserv
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                                                                                                                                                    PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                     Nematoda;
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                                                                                                                                                                                                                                                                                               Caenorhabditis
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Last sequence update)
Last annotation update)
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Pred. No. 9
                                                                                                                                                                                                                                                                                                                              Chromadorea;
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phosphorylates co
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                                                                              Consortium
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Best Local S
Matches 160
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Interpro; IPR002488; Death.
Interpro; IPR002719; Euk_pkinase.
Interpro; IPR002719; Ser_thr_pkinase.
Interpro; IPR002719; Ser_thr_pkinase.
Interpro; IPR002719; Ser_thr_pkinase.
Interpro; IPR002719; Ser_thr.
Interpro; IPR002719; Ser_thr.
Interpro; IPR002719; Ser_thr.
Interpro; IPR002719; ANK; 7.
INTERPROSITE; SM002719; SMART; 1.
INTERPRESITE; PS50088; ANK_REPEAT; 7.
INTERPROSITE; PS50017; DEATH_DOMAIN; 1.
INTERPROSITE; PS50017; DEATH_DOMAIN; 1.
INTERPRESITE; PS50018; PROTEIN_KINASE_DOM; 1.
INTERPRESITE; PS50019; PROTEIN_KINASE_ST; 1.
INTERPRESITE; PS50019; PROTEIN_KINASE_ST; 1.
INTERPRESITE; PS50019; PROTEIN_KINASE_ST; 1.
INTERPRESITE; PS50019; PROTEIN_KINASE_ST; 1.
INTERPRESITED
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Submitted (MAR-2001) t
Submitted 1: SIMILARITY: BELONG
1- SIMILARITY: BELONG
EMBL; AF043701; AAK189
HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted [3]
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"The sequence of C. 6
Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                Q9C0L5;
01-JUN-2001 (
01-JUN-2001 (
01-DEC-2001 (
MYOSIN LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase
SEQUENCE
  Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                       Q9C0L5
                                                                                                                                                                                                                                                                                                                   140
                         MLCK.
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                                                                                                                                            378
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                                                                                                                                                                                                                               KPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYEPLGLEADM
                                                                                                                                                                                                                                                                                                                  AVYETASDVIIVLELVSGGELFDHVCAKECLDEVEAAAFIKQILLAVRHLHSLHIVHLDI
                                                                                                                                                                                    KPENVML--KQRGDSQIKIIDFGLSREIEPGAVVKDMVGTPEFVAPEVVNYEALSPATDM
                                                                                                                                           SLMKKVHLRPDED -- LRNCESDTEEDIARRKALH
                                                                                                                                                                                                                                                                                                                                                                                                        160;
                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1435 AA; 160602 MW;
                                  1 (TrEMBLrel. 17, 1 (TrEMBLrel. 17, 1 (TrEMBLrel. 19, 1 (TrEMBLrel. 19, 17))
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001) to the EMBL/GenBank/DDBJ
BELONGS TO THE SER/THR FAMILY
BAK18971.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . elegans
8) to the
                                                                                                                                                                                                                                                                                                                                                                                                                  42.68;
      Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cosmid K12C11.";
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 787; DB 5;
Pred. No. 1.7e-48;
                                                                      Created)
                                                Last sequence update)
Last annotation updat
                                                                                            PRT;
        Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               C73EB605C37FB732 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine/threonine-protein
                                                                                                                                                                      352
          Vertebrata;
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OF PROTEIN
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                                                 update)
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           Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                               6
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4.

macaque

brain

CDNA

databases OF PROTEIN

KINASES

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RESULT
Q9BE69
ID Q9
AC QC
DT 01
DT 01
DT 01
OS M
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Best Local Similarity
Matches 146; Conserv
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R Pfam; PF00067; 19; 2.

R Pfam; PF00069; pkinase; 1.

R Pfam; PF00069; pkinase; 1.

R PRINTS; PR00014; ENTYPEIII.

R SMART; SM00408; IGC2; 3.

R SMART; SM00408; IGC2; 3.

R SMART; SM00220; S_TKC; 1.

R SMART; SM00219; TyrKC; 1.

R SMART; SM00219; TyrKC; 1.

R PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

R PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

R PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

R PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

W ATP-binding; Immunoglobulin domain; Kinase; Repeat;

Serine/threonine-protein kinase; Transferase.

SEQUENCE 992 AA; 110185 MW; 3A8D772460983269 CRC64
     Q9BE69 PRELIMINARY; PRT; 641 AA. Q9BE69; O1-JUN-2001 (TrEMBLrel. 17, Created) O1-JUN-2001 (TrEMBLrel. 17, Last sequence update) O1-DEC-2001 (TrEMBLrel. 19, Last annotation update) HYPOTHETICAL 72.2 KDA PROTEIN.
HYPOTHETICAL 72.2 KDA PROTEIN margague) (Cynomolg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "HeLa myosin light chain kinase.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY
EMBL; AB037663; BAB21504.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
InterPro;
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NCBI_TaxID=9606;
                                                                                                                                                                                                                   822
                                                                                                                                                                                                                                                         304
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                                                                                                                                                                                                                 KWQKTGNAVRAIGRLSSMAMISGLSGRKSSTGSPTSPLNAEKLESEEDVSQ
                                                                                                                                                                                                                                                                                                                                                                   DGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREV 65
                                                                                                                                                                                                                                                     RWKLSFSIVSLCNHLTRSLM-----KKVHLRPDEDLRNCESDTEEDIAR
                                                                                                                                                                                                                                                                                                                 SELAKDFIRKLLVKETRKRLTIQEALRHPWI-TPVDNQQAMVRRESVVNLENFRKQYVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMNCLHHPKLVQCVDAFEEKANIVMVLEIVSGGELFERIIDEDFELTERECIKYMRQIS 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQKVSDFYDIEERLGSGKFGQVFRLVEKKTRKVWAGKFFKAYSAK-----EKENIRQEI 588
                                                                                                                                                                                                                                                                                           SDDAKDFISNLLKKDMKNRLDCTQCLQHPWLMKDTKNMEA----KKLSKDRMKKYMARR
                                                                                                                                                                                                                                                                                                                                                                                                                                              EGVEYTHKQGIVHLDLKPENIMCVNKT--GTRIKLIDFGLARRLENAGSLKVLFGTPEFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQIL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003962;
IPR003961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR002290;
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IPR003006;
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962; FnIII_repeat.
961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Ig.
; Ig_c2.
; Ig_MHC.
; Ser_thr_pkinase.
; Tyr_pkinase.
(Crab eating macaque) (Cynomolgus monkey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.8%;
41.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 698; DB 4
Pred. No. 3e-42;
6; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                 872
                                                                                                                                                                                                                                                     347
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RESULT
Q98850
ID Q98
AC Q98
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DT 01-
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Best Local Similarity 41.0
Matches 146; Conservative
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InterPro; IPR003600; Ig_like.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00041; fn3; 1.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00014; FNTYPEIII.
SNART; SN00060; FN3; 1.
SNART; SN00409; IG; 1.
SNART; SN00410; IG_like; 1.
SNART; SN00420; STRG; 1.
SNART; SN00210; STRG; 1.
SNART; SN00210; TyrKc; 1.
SNART; SN00210; TyrKc; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; PROTEIN_KINASE_ST; PROTEI
Q98850;
Q98850;
01:FEB-1997
01-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003962; FnIII repeat.
InterPro; IPR003961; FnIII.
InterPro; IPR003599; Ig.
InterPro; IPR003500; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2001) to the EMBL/GenBank/DDBJ

-- SIMILARITY: BELONGS TO THE SER/THR FAMILY

EMBL; AB056801; BAB39325.1; --

EMBL; AB056801; BAB39325.1; --

HSSP; P56276; ITLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=FRONTAL LOBE LEFT;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   libraries."
                                                                                                                                                         544
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                                                                                                                                                                                                                                                                                                             429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311
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                                                                                                                                                                                         304 RWKLSFSIVSLCNHLTRSLM-----KKVHLRPDEDLRNCESDTEEDIAR 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQIL 124
                                                                                                                                                                                                                                                                                                                                 APEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHT
                                                                                                                                                                                                                                                                                                                                                                                                           DGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQKVSDVYDIEERLGSGKFGQVFRLVEKKTRKIWAGKFFKAYSAK-----EKENIRQEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGVEYIHKQGIVHLDLKPENIMCVNKT--GTRIKLIDFGLARRLEDAGSLKVLFGTPEFV
                                                                                                                                                         KWQKTGNAVRAIGRLSSMAMISGLSGRKSSTGSPTSPLNAEKLESEEDVSQ
                                                                                                                                                                                                                                 SDDAKDFISNLLKKDMKNRLDCTQCLQHPWLMKDTKNMEA---
                                                                                                                                                                                                                                                                     SELAKDFIRKLLVKETRKRLTIQEALRHPWI-TPVDNQQAMVRRESVVNLENFRKQYVRR 303
                                                                                                                                                                                                                                                                                                             APEVINYEPIGYATDMWSIGVICYILVSGLSPFMGDNDNETLANVTSATWDFDDEAFDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    641 AA;
(TrEMBLrel.
                                                         PRĘLIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72195 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.6%;
02,
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Created)
Last sequ
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Pred. No. 2.8e-42;
5; Mismatches 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Cercopithecidae;
                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48BAA0621851868E
 sequence update)
                                                           907
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118;

Indels

22;

Gaps

6

310

184 370

244 428 Length

641;

CRC64;

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R InterPro; iPRO02290; Ser_thr_pkinase.

R pfam; pF00041; fn3; 1.

R pfam; pF00041; fn3; 1.

R pfam; pF00069; pkinase; 1.

R smART; SM00060; FN3; 1.

R SMART; SM00060; FN3; 1.

R SMART; SM00108; iGc2; 2.

R SMART; SM001010; pROTEIN_KINASE_ATP; UNKNOWN_1.

R PROSITE; PS00101; pROTEIN_KINASE_DOM; 1.

R PROSITE; PS00108; PROTEIN_KINASE_T; 1.

R PROSITE; PS00108; PROTEIN_KINASE, ST; 1.

R PROSITE; PS00108; PROTEIN_KINASE, ST; 1.

R PROSITE; PS00108; PROTEIN_KINASE; Transferase; Serine/threonine-protein kinase; Transferase.

SECTION-Christian Structure of the protein kinase; Transferase.
                                                      RESULT
Q91XS9
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 BBBB
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Best Local
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Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFMLCK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Last annotation NEURONAL MYOSIN LIGHT CHAIN KINASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             during axon regeneration.";
Neurobiol. 31:379-391(1996).
1: SIMILARITY: BELONGS TO THE SER/THR
EMBL; U61731; AAB41402.1;
HSSP; P56276; ITLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97067382; PubMed-8910795;
Jian X., Szaro B.G., Schmidt J.T.;
"Myosin light chain kinase: expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-COMMON COMET;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carassius auratus (Goldfish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000719; Euk_pkinase.
Interpro; IPR003961; FN_III.
Interpro; IPR003598; I9_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-7957;
Q91XS9;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                        465
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                                         Q91XS9
                                                                                                                                                                                                                                                            187
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                                                                                                                                                                                                                                                                                                                                                                                                       KVKDLYDVEDRLGTGKFGAVFKLIEKSTKKVWAGKFIKAYSAK-----EKDNVRQEIAI
                                                                                                                                                                                                                                                                                                                                                                                                                               KVEDFYDIGEELGSGOFAIVKKCREKSTGLEYAAKFIKKROSRASRRGVSREEIEREVSI
                                                                                                                                                                                                                                                                                                                                               VNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAP 186
                                                                                                                                                                                                  LAKDETRKLLVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLENFRKQYVRRRWK 306
                                                                                                                                                                                                                               EIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSE
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                                                                                                                                                                                                                                                                                       VSFTHKKGIVHLDLKPENINCVNKT--GSKIKLIDFGLARRLENAGSLKVLFGTPEFVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
141; Conserv
                                                                                                                 KTGHAVRAIGRLSNMALLAGVHAKKG-----SPTEED
                                                                                                                                           LSFSIVSLCNHLTR-SLMKKVHLRPDEDLRNCESDTEED 344
                                                                                                                                                                       EAKDFISNLLKKDMKARLSCDQCFQHPWLKQ-DTTNMEVKK----LSKERMKKYILRRKWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
   (TrEMBLrel.
                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.3%;
      19,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 688.5; DB
Pred. No. 1.3e-41
    Created)
Last sequ
                                                 PRT;
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       sequence
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                                                   611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
Euteleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurons and
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                                                    A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107;
          update)
                                                                                                                          784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Search completed: May 18, Job time: 1449 sec

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Best Local S
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NON_TER
SEQUENCE
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Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Hystricognathi; Caviidae; Cavia.
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=BASAL ARTERY;
Makamura A., Liu L., Hanyuda Y., Kohama K.;
Makamura Cloning of myosin light chain kinase of the 'myolecular cloning of myosin light chain kinase of the from Guinea Pig vascular smooth muscle.";
from Guinea Pig vascular smooth muscle.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases Submitted (AUG-2001) to the EMBL/AgenBank/DBBJ databases EMBL; AB070227; BAB63286.1; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                            Kinase.
                                                                                                                                                   430
                                                                                                                                                                                                    316
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                                                                                                                                                              125 DGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFV 184
                                                                                                  488
                                                548
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                                                                                                                                                                                                                 66 SILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKOIL 124
603
                        304
                                                                                                                                                                                                                                                                           6 QQKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREV
                                                                                                                                                                                                                                                     APEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHT 244
                                                                                                  EGVEYIHKQGIVHLDLKPENIMCVNKT--GTRIKLIDFGLARRLENAGSLKVLFGTPEFV
: | :
                        RWK
                                                              SELAKDFIRKLLVKETRKRLTIQEALRHPWI-TPVDNQQAMVRRESVVNLENFRKQYVRR 303
                                                SEDAKDFISNMLKKDMKNRLNCTECLQHPWLMKDTKNMEA-----KKLSKDRMKKYMARR
                                                                                                                                                                                                                                                                                                                      Similarity
                          306
 605
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                        AA;
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611
68810 MW;
                                                                                                                                                                                                                                                                                                                      36.2%; Score 668.5;
44.2%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                             56;
                                                                                                                                                                                                                                                                                                                                                                         14B6EF874BE6A7F5 CRC64;
                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                                                                                 98;
                                                                                                                                                                                                                                                                                                                  Indels
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